

# SEQUENCE LISTING

<110> Wright, David A.  
Voytas, Daniel F.

<120> Plant Retroelements and Methods Related Thereto

<130> P-1065 ISURF Plant Retroelement

<140> unknown

<141> 1999-05-28

<150> 60/087125

<151> 1998-05-29

<160> 42

<170> PatentIn Ver. 2.0

<210> 1

<211> 18

<212> DNA

<213> Glycine max

<400> 1

tggcgcgctt gccaatg

18

<210> 2

<211> 18

<212> DNA

<213> Glycine max

<400> 2

tggcgcgctt gtcgggga

18

<210> 3

<211> 6

<212> DNA

<213> Glycine max

<400> 3

ttgggg

6

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 4

Met Ala Ser Arg Lys Arg Lys

1

5

<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 5

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tcacgtttca ctttcgagat tgcttggcac agataccagg atagcattca gctccggaac 120  
atccttccag agaggaatgt agagcttggg ccagggatgt ttgatgagtt cctgcaggaa 180  
ctccagaggc tcagatggga ccaggttctg acccgacttc cagagaagtg gattgatgtt 240  
gctctggtga aggagtttta ctccaaccta tatgatccag aggaccacag tccgaagttt 300  
tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac 360  
accccggtca tcttggcaga gggagaggat tatccagcct actctcagta cctcagcaact 420  
cctccagacc atgatgccat ctttccgct ctgtgtactc cagggggacg atttgttctg 480  
aatgttgata gtgccccctg gaagctgctg cggaaggatc tgatgacgct cgcgagaca 540  
tggagtgtgc tctcttattt taaccttgca ctgacttttc acacttctga tattaatgtt 600  
gacagggccc gactcaatta tggcttgggt atgaagatgg acctggacgt gggcagcctc 660  
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tga 1263

<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 6

Met Ala Ser Arg Lys Arg Lys Ala Val Pro Thr Pro Gly Glu Ala Ser

1

5

10

15

Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr  
                   20                                  25                                  30

Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu  
                   35                                  40                                  45

Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu  
                   50                                  55                                  60

Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val  
                   65                                  70                                  75                                  80

Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His  
                                   85                                  90                                  95

Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala  
                                   100                                  105                                  110

Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly  
                   115                                  120                                  125

Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His  
                   130                                  135                                  140

Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu  
                   145                                  150                                  155                                  160

Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr  
                                   165                                  170                                  175

Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr  
                   180                                  185                                  190

Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly  
                   195                                  200                                  205

Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln  
                   210                                  215                                  220

Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala  
                   225                                  230                                  235                                  240

Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu  
                   245                                  250                                  255

Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys  
                   260                                  265                                  270

Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg  
                   275                                  280                                  285

Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro  
290 295 300

Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu  
305 310 315 320

Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser  
325 330 335

Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser  
340 345 350

Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg  
355 360 365

Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu  
370 375 380

Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp  
385 390 395 400

Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu  
405 410 415

Gly Arg Gly Ser Glx  
420

<210> 7

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 7

atgcgaggta gaactgcata tggagacgtt gttcctatta acttagaaat tgaagctacg 60  
tgtcggcgta acaacgctgc aagaagaaga agggagcaag acatagaagg aagtagttac 120  
acctcacctc ctctttctcc aaattatgct cagatggacg gggaaccggc acaaagagtc 180  
acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg 240  
gaagtccaag cagatctcct tactcaaggg aacctcttcc atggtcttcc aaatgaagat 300  
ccatatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt 360  
ccaaaagatg cgatactcct taacctcttt tccttttccc tagcaggaga ggcaaaaaga 420  
tggttgcaact cctttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480  
ttaaagaagt atttccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc 540  
catcaatttc tggatgaatc ccttagcgaa gcaactagacc atttccacgg attgctaaga 600  
aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660  
caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720

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atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat 780
gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac 840
aagctgttga cgaggcagat agaagccctc atcgaaaccc tcagcaagct gcctcaacaa 900
ttacaagcga taagttcttc ccaactcttc gttttgcagg tagaagaatg ccccatatgc 960
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ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggtttaatca aggaagaaac 1140
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ccaccatacc agccaccata ccagcaccct agccaaggtc cgaatcagca agaaaagccc 1260
acaaaatag aggaactgct gctgcaattc atcaaggaga caagatcaca tcaaaagagc 1320
acggatgcag ccattcgga tctagaagtt caaatgggccc aactggcgca tgacaaagcc 1380
gaacggccca ctagaacttt cgggtgcta ac atggagagaa gaaccccaag gaaggataaa 1440
gcagtactga ctagagggca gagaagagcg caggaggagg gtaagggttg aggagaagac 1500
tggccagaag aaggaaggac agagaagaca gaagaagaag agaagggtggc agaagaacct 1560
aagcgtacca agagccagag agcaaggga gccaag 1596

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<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 8

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Met Arg Gly Arg Thr Ala Ser Gly Asp Val Val Pro Ile Asn Leu Glu
  1             5             10             15

Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu
      20             25             30

Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn
      35             40             45

Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp
      50             55             60

Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
      65             70             75             80

Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
      85             90             95

Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
      100            105            110

Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
      115            120            125

Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser

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130	135	140
Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe		
145	150	155 160
Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu		
165	170	175
Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu		
180	185	190
Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser		
195	200	205
Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile		
210	215	220
Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala		
225	230	235 240
Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His		
245	250	255
Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr		
260	265	270
Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu		
275	280	285
Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile		
290	295	300
Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys		
305	310	315 320
Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser		
325	330	335
Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly		
340	345	350
Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe		
355	360	365
Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly		
370	375	380
Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln		
385	390	395 400
Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln		

405

410

415

Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys  
420 425 430

Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu  
435 440 445

Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr  
450 455 460

Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys  
465 470 475 480

Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val  
485 490 495

Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu  
500 505 510

Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala  
515 520 525

Arg Glu Ala Lys  
530

<210> 9

<211> 603

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 9

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atcatggaag tagagatctt tgactgttgg ggcatagact tcatggggcc ttttccttcg 120  
tcatacggga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc 180  
atagccacgc caaaggacga tgccagggta gtgatcaaat ttctgaagaa gaacattttt 240  
tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat 300  
cagttgaaga aagtccctgga gcactataat gtccgacata aggtggccac accttatcac 360  
cctcagacaa atggccaagc agaaatttct aacaggggagc tcaagcgaat cctggaaaag 420  
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480  
aggacagcgt tcaagactcc catcggtta tcaccatttc agctagtgtg tgggaaggca 540  
tgtcatttac cagtggagct ggagtacaaa gcatattggg ctctcaagtt gctcaacttt 600  
gac 603

<210> 10

<211> 201

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 10

Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met  
1 5 10 15

Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile  
20 25 30

Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu  
35 40 45

Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro  
50 55 60

Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe  
65 70 75 80

Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His  
85 90 95

Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg  
100 105 110

His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu  
115 120 125

Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser  
130 135 140

Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr  
145 150 155 160

Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val  
165 170 175

Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr  
180 185 190

Trp Ala Leu Lys Leu Leu Asn Phe Asp  
195 200

<210> 11

<211> 600



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 11  
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gttcccaaga aagggtggaat gacagtggta cgagatgaga ggaatgactt gataccaaca 120  
cgaactgtca ctggttggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180  
aaggaccatt tcccccttacc ttccatggat cagatgctgg agagacttgc agggcaggca 240  
tactactggt tcttggatgg atactcggga tacaaccaga tcgcggtaga cccagagat 300  
caggagaaga cggcctttac atgccccctt ggcgtctttg cttacagaag gatgccattc 360  
gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg 420  
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac 480  
agctgtttga ggaacctaga gaggtactt cagaggtgcg aagagactaa cttggtactg 540  
aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca 600

<210> 12  
<211> 200  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 12  
Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser Ala Trp Val Ser  
1 5 10 15  
Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp  
20 25 30  
Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met  
35 40 45  
Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe  
50 55 60  
Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu Ala Gly Gln Ala  
65 70 75 80  
Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ala Val  
85 90 95  
Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys Pro Phe Gly Val  
100 105 110  
Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr

115	120	125
Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met Val Glu Lys Ser		
130	135	140
Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly Pro Ser Phe Asp		
145	150	155 160
Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg Cys Glu Glu Thr		
165	170	175
Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Arg Glu Gly		
180	185	190
Ile Val Leu Gly His Lys Ile Ser		
195	200	

<210> 13  
 <211> 858  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 13  
 aaggaagaac cactagccct tccacaggat ctcccatatc ctatggcacc caccaagaag 60  
 aacaaggagc gttactttgc acgtttcttg gaaatattca aagggttaga aatcactatg 120  
 ccattcgggg aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc 180  
 accaagaagg ggaagtatat tgacaacgag aatattgtgg taggaggcaa ttgcagtgcg 240  
 ataatacaaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccgtgc 300  
 accattggga aggaagccgt aaacaaggcc ctcatgtatc taggagcaag tatcaatctg 360  
 atgcccttgt caatgtgcaa aagaattggg aatttgaaga tagatcccac caagatgacg 420  
 ctccaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgtcctgggc 480  
 aaggtacgcc acttcacttt tccgggtggac tttgttatca tggatatcga agaagacact 540  
 gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600  
 gggaaaggga acttagagtt gactattgat aatcagaaga tcacctttga ccttatcaag 660  
 gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa 720  
 gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggt aaatcattta 780  
 gactgtctaa ccagtgaaga ggaagaagat ctgaaggctt gcttggaaaa cttggatcaa 840  
 gaagacagta ttcctgag 858

<210> 14  
 <211> 286  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: plant

retroelement sequence

<400> 14

Lys Glu Glu Pro Leu Ala Leu Pro Gln Asp Leu Pro Tyr Pro Met Ala  
 1 5 10 15

Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile  
 20 25 30

Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln  
 35 40 45

Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly  
 50 55 60

Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala  
 65 70 75 80

Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val  
 85 90 95

Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile  
 100 105 110

Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg  
 115 120 125

Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala  
 130 135 140

Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val  
 145 150 155 160

Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile  
 165 170 175

Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu  
 180 185 190

Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr  
 195 200 205

Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr  
 210 215 220

Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu  
 225 230 235 240

Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met  
 245 250 255

Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys  
 260 265 270

Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu  
 275 280 285

<210> 15

<211> 192

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 15

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 gacaaggat ttcacgccat ctattatgct agcaaggccc tgaatgaagc acagttgaat 120  
 tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttggagaa gttcagggtca 180  
 tacttgatag gg 192

<210> 16

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
 retroelement sequence

<400> 16

Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Val Gly Ala Val Leu  
 1 5 10 15

Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys  
 20 25 30

Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met  
 35 40 45

Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly  
 50 55 60

<210> 17

<211> 12286

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: plant  
retroelement sequence

<400> 17

tgataactgc taaataattg tgaattaata gtagaaaatt agtcaaattt tggcttaaaa 60  
ttaattattht agcagttatt tgtgattaaa agttagaaaa gcaattaagt tgaattttttg 120  
gccatagata tgaaaactga aggtacaaca agcaaaaggc agcagaaagt gaagaaaaag 180  
aataaaaatct gaagcagacc cagccaaca cgcgccctta gcgcgcgtca cgcgcctaagc 240  
ttgcaaggca gcacaggcac taagcgaggc gttaagcacg aagatgcagg attcgttacg 300  
tgcgctaagc gcgaggcaca cgctaagcgc gcgatccaac agaagcacac gctaagcctg 360  
cagcatgcmc taagcgcgcc tacgaaggcc caaagcccat ttctacacct ataaatagag 420  
atccaagcca agggagaatg tacaccttgc ctcagagcac ttctctcagc attccaagct 480  
tgagctctcc cttttctctc tatattcttt gcttttatta tccattcttt ctttcacccc 540  
agttgtaaaag cccctcaatg gccatgagtg gttaatcccc tagctacggc ctggtaggcc 600  
taaaaagcca atgatgtatg gtgtacttca agagttatca atgcaaagag gattcattcc 660  
aggttttatg ttctaattct ttccctttta tottgcattht atgtcttaaa tttctgttg 720  
gtttttattcg ctcgggagag ggtatttctc aataagggtt taagaagtaa tgcattgcac 780  
agtttttaggg gttatacgtc ttgttaaagg taacacctaa tagaacaat taagaaaagg 840  
atcgtcgggc tagcattgct aggcatagaa tgatggccca atgcccatgc atttagcaac 900  
atctagaatt taaccttaat gcattttaat tattgaatct tcacaaaggc atttgggaga 960  
taggtagtta aaataggctt gtcactgtga ggcattcaagg gcaagtataa ttaatagatg 1020  
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Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp  
 50 55 60

Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro  
 65 70 75 80

Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu  
 85 90 95

Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys  
 100 105 110

Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn  
 115 120 125

Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser  
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Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe  
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Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu  
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 Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu  
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 Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser  
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 Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His  
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 Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr  
 260 265 270  
 Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu  
 275 280 285  
 Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile  
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 Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys  
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 Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly  
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 Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe  
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 Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly  
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 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln  
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 Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys

420

425

430

Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu  
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Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr  
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Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys  
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Tyr Pro Met Ala Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg  
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Phe Leu Glu Ile Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu  
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Ala Leu Gln Gln Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu  
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Thr Lys Lys Gly Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly  
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Asn Cys Ser Ala Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp  
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Pro Gly Ser Val Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn  
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Lys Ala Leu Ile Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser  
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Met Cys Lys Arg Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr  
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Asp Val Leu Val Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val			
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Ile Met Asp Ile Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg			
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Pro Phe Met Leu Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn			
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Leu Glu Leu Thr Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys			
	740	745	750
Ala Met Lys Tyr Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu			
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Ile Asp Glu Glu Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu			
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Glu Lys Ala Met Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu			
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Glu Asp Leu Lys Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile			
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Pro Glu Gly Glu Ala Asn Phe Glu Glu Leu Glu Lys Glu Val Pro Ser			
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Glu Lys Pro Lys Ile Glu Leu Lys Ile Leu Pro Asp His Leu Lys Tyr			
	835	840	845
Val Phe Leu Glu Glu Asp Lys Pro Ile Val Ile Ser Asn Ala Leu Thr			
	850	855	860
Thr Glu Glu Glu Asn Arg Leu Val Asp Val Leu Lys Lys His Arg Glu			
	865	870	875
Ala Ile Gly Trp His Ile Ser Asp Leu Lys Glu Ile Ser Pro Ala Tyr			
	885	890	895
Cys Met His Arg Ile Met Met Glu Glu Asp Tyr Lys Pro Val Arg Gln			
	900	905	910
Pro Gln Arg Arg Leu Asn Pro Thr Met Lys Glu Glu Val Arg Lys Glu			
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Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro Ile Ser Asp Ser			
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Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr			
	945	950	955
			960

Val Val Arg Asp Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr	965	970	975
Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg	980	985	990
Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu	995	1000	1005
Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn	1010	1015	1020
Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys	1025	1030	1035
Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn	1045	1050	1055
Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met	1060	1065	1070
Val Glu Lys Ser Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly	1075	1080	1085
Pro Ser Phe Asp Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg	1090	1095	1100
Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met	1105	1110	1115
Val Arg Glu Gly Ile Val Leu Gly His Lys Ile Ser Ala Arg Gly Ile	1125	1130	1135
Glu Val Asp Arg Ala Lys Ile Asp Val Ile Glu Lys Leu Pro Pro Pro	1140	1145	1150
Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His Ala Gly Phe Tyr	1155	1160	1165
Arg Arg Phe Ile Lys Asp Phe Ser Lys Ile Ala Arg Pro Leu Ser Asn	1170	1175	1180
Leu Leu Asn Lys Asp Val Ala Phe Val Phe Asp Glu Glu Cys Leu Ala	1185	1190	1195
Ala Phe Gln Ser Leu Lys Asn Lys Leu Val Thr Ala Pro Val Met Ile	1205	1210	1215
Ala Pro Asp Trp Asn Lys Asp Phe Glu Leu Met Cys Asp Ala Ser Asp	1220	1225	1230

Tyr Ala Val Gly Ala Val Leu Gly Gln Arg Lys Asp Lys Val Phe His  
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Ala Thr Thr Glu Lys Glu Met Leu Ala Ile Val Phe Ala Leu Glu Lys  
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Phe Arg Ser Tyr Leu Ile Gly Ser Arg Val Ile Ile Tyr Thr Asp His  
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Ala Ala Ile Lys His Leu Leu Ala Lys Thr Asp Ser Lys Pro Arg Leu  
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Ile Arg Trp Val Leu Leu Leu Gln Glu Phe Asp Ile Ile Ile Lys Asp  
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Lys Lys Gly Ser Glu Asn Val Val Ala Asn His Leu Ser Arg Leu Lys  
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Asn Glu Glu Val Thr Lys Glu Glu Pro Glu Val Lys Gly Glu Phe Pro  
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Pro His Leu Phe Lys Ala Gly Ala Asp Asn Leu Leu Arg Arg Cys Val  
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Thr Lys Glu Glu Ala Arg Ser Ile Leu Trp His Cys His Ser Ser Pro  
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Tyr Gly Gly His His Ser Gly Asp Arg Thr Ala Ala Lys Val Leu Gln  
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Ser Gly Phe Phe Trp Pro Ser Ile Phe Lys Asp Ala His Glu Phe Val  
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Val Arg His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln  
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Ala Glu Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val  
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<210> 24

<211> 1857

<212> DNA

<213> Arabidopsis thaliana

<400> 24

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<210> 25

<211> 1254



<212> DNA

<213> *Pisum sativum*

<400> 25

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ttggaaaagc gaaagatttt gccggaaaag agatttataa tcaaccctga aggcacgaac 180
cgtacattcg ccgggctgat taacagcaaa aagtgggacc ggttaatatc ccccttgaag 240
cattacgaca tcgcaacagt gcgtgagttc tacgcgaacg cactgccgaa cgacgacgag 300
ccattcacat ggacgtctag agtgtccggc cgtcctggtg cgttcgatcg ggatgcaatt 360
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<210> 26

<211> 564

<212> DNA

<213> *Arabidopsis thaliana*

<400> 26

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tcatacggta ataaatatat actggtcgcc gtagactacg tatcaaagtg ggtcgaagct 180
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gtttttgaga acctcttgaa gaagcatggg gtaaagcagg ttgagatctc caatagggag 360
ataaaaacaa ttctggaaaa gactgttggg attacaagga aagactggtc tgcaaaagcta 420
gatgatgcat tatgggctta caggacagct ttcaagacct ccataggtac aactcctttc 480
aatcttctct atggaaaatt atgtcatcta cccgttgagc tcgagtacaa agcaatgtgg 540
gcggtaaaac ttctgaactt tgac 564
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<210> 27

<211> 600

<212> DNA

<213> *Arabidopsis thaliana*

<400> 27

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cttgatgctg gtgtcatcta ccctatctct gatagtactt gggtttctcc agtgcattgc 60
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```

agaactataa ctggtcata aatgtgcata gattatagga agttgaacgc tgcattctagg 180
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```

<210> 28

<211> 192

<212> DNA

<213> *Arabidopsis thaliana*

<400> 28

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tttgaaatca tgtgtgatgc atcagattac gcagtaggag ctgttctagg ccagaaaata 60
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tatgcaacaa ctgagaagga gcttctagct gttgtattcg catttgagaa gttcagaagc 180
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<210> 29

<211> 597

<212> DNA

<213> *Pisum sativum*

<400> 29

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aaagttgcaa cggggtggag aatgtgtatt gaatataggc ggttgaatac cgcaactcga 180
aaggaccatt ttccactccc gtcatggat caaatgctgg aaagactctc cgggcaacaa 240
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ttatgcttgg caaacttgaa aacggtgctt gaaagatgtg tgaagaccaa tcttgtgctt 540
aattggtaga agtgccactt catggtgacc gaggggatag tgcttgacca taaagtc 597

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<210> 30

<211> 192

<212> DNA

<213> *Pisum sativum*

<400> 30

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tttgagctaa tgtgtgatgc gagcaactat gcaatcggag cgggtattagg ccaaagaaaa 60
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tatgccacca ctgaaaaaga attacttgcg atagtgtatg cacttgaaaa gtttaggtct 180
tatcttatag gg 192

```

<210> 31

<211> 581

<212> DNA

<213> Pisum sativum

<400> 31

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<210> 32

<211> 1362

<212> DNA

<213> Glycine max

<400> 32

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<210> 33

<211> 192

<212> DNA

<213> Glycine max

<400> 33

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tatgctacca cagaaaaaga aatgTTggca attgTTtatg cacttgaaaa gttcaaattct 180  
tatttggtag gc 192

<210> 34

<211> 597

<212> DNA

<213> Glycine max

<400> 34

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<210> 35

<211> 603

<212> DNA

<213> Glycine max

<400> 35

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aggacagcgt tcaagactcc catcggtta tcaccatttc agctagtata tgggaaggca 540  
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gac 603

<210> 36

<211> 150

<212> DNA

<213> Glycine max

<400> 36

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tagatcaagt tctttttcaa tttctttttt 150

<210> 37

<211> 11  
<212> DNA  
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<400> 37  
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11

<210> 38  
<211> 15  
<212> DNA  
<213> Glycine max

<400> 38  
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15

<210> 39  
<211> 27  
<212> DNA  
<213> Glycine max

<400> 39  
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27

<210> 40  
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<212> DNA  
<213> Glycine max

<400> 40  
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9

<210> 41  
<211> 16  
<212> DNA  
<213> Glycine max

<400> 41  
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16